

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: April 1, 2006, 04:15:51 ; Search time 2046 Seconds
(without alignments)

2361.531 Million cell updates/sec

Title: US-10-767-609-1

Perfect score: 85

Sequence: 1 gtgagtgtgttagttc.....gcacctatttcattgttcag 85

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_on.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_ey.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	85	6	AX025268 Sequence
2	85	100.0	103	1	S74256 rola-transf
3	85	100.0	700	15	X76001 A.thaliana
4	85	100.0	720	1	X12579 Agrobacteri
5	85	100.0	831	11	AF442734 Synthetic
6	85	100.0	831	11	AF442735 Synthetic
7	85	100.0	21126	1	R1ATL
8	85	100.0	21126	6	AR050120
9	85	100.0	21126	6	I04770 Sequence 94
10	85	100.0	21126	6	I24453 Sequence 19
11	77	90.6	86	6	AX078800
12	35.8	42.1	167978	8	AC096914
13	35.8	42.1	193384	14	AC021057
14	35.8	42.1	275519	14	AC119596
15	35.6	41.9	141016	14	AC148204
16	35.6	41.9	179882	14	AC159168
17	34.2	40.2	236039	14	AC121212
18	34	40.0	105707	5	BX950225 Zebratfish

c 19 33.8 39.8 188633 9 AC159301
 c 20 33.4 39.3 110000 15 CR382134_09
 c 21 33.4 39.3 110000 15 CR382134_10
 c 22 33.4 39.3 174655 8 AC023347
 c 23 33.4 39.3 246322 14 AC133966
 c 24 33 38.8 1407 6 AX416421
 c 25 33 38.8 187145 14 CR626902
 c 26 33 38.8 290683 1 AE017329
 c 27 33 38.8 295050 1 AL591982
 c 28 33 38.8 349980 6 AX641671
 c 29 32.8 38.6 116909 15 AC157349
 c 30 32.4 38.1 153106 14 AC162469
 c 31 32.4 38.1 170456 14 AC144751
 c 32 32.4 38.1 203456 14 AC144999
 c 33 32.4 38.1 337101 8 HSKSRPXR
 c 34 32.4 38.1 349980 6 AX344555
 c 35 32.2 37.9 78245 5 BX950855
 c 36 32.2 37.9 161001 8 AC068775
 c 37 32.2 37.9 188938 14 AC119064
 c 38 32.2 37.9 195551 14 AC006281
 c 39 32.2 37.9 218834 14 AC105640
 c 40 32.2 37.9 226994 14 AC128720
 c 41 32.2 37.9 251551 2 AE014844
 c 42 32.2 37.9 319223 14 AC128879
 c 43 32 37.6 659 10 BV253440
 c 44 32 37.6 6031 6 AX323720
 c 45 32 37.6 125987 15 CT009553

ALIGNMENTS

RESULT 1
 AX025268
 LOCUS AX025268 85 bp DNA linear PAT 16-SEP-2000
 DEFINITION Sequence 1 from Patent EP1002868.
 ACCESSION AX025268
 VERSION AX025268.1 GI:10186982
 KEYWORDS
 SOURCE Agrobacterium rhizogenes (Rhizobium rhizogenes)
 ORGANISM Agrobacterium rhizogenes
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Rhizobiaceae; Agrobacterium.

REFERENCE

1 Defez, R. and Spena, A.

AUTHORS

TITLE

Method to control gene expression in bacteria namely rhizobiaceae

to improve root nodule development nitrogen fixation and plant

biomass production

JOURNAL

Patent: EP 1002868-A 1 24-MAY-2000;

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(IT)

FEATURES

source

1. .85

/organism="Agrobacterium rhizogenes"

/mol_type="unassigned DNA"

/db_xref="taxon:359"

ORIGIN

Query Match 100.0%; Score 85; DB 6; Length 85;

Best Local Similarity 100.0%; Pred. No. 7.3e-09;

Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGAGTGTGTTGAGTTCAATTATTTTACATTTTTCAGCTGTGTTTCCCTTTTCT 60

Db 1 GTGAGTGTGTTGAGTTCAATTATTTTACATTTTTCAGCTGTGTTTCCCTTTTCT 60

Qy 61 AATATGACCTATTTCATGTTTCAG 85

Db 61 AATATGACCTATTTCATGTTTCAG 85

RESULT 2

S74256